Fig. 1

```
1        CCAGATTCCCATAAAGCACATGGTCTAATCTGTTACGTAACAGCAAGACA   50
51   GCGTCACCTCACCTGTTCTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAG  109
110  ACCACCAGGCTGAGTATCCTGACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGG  168
169  GAACCTTCCATTATATTCTTCAAGCAACTTACAGCTGCACCGACAGTTGCG ATG AAA  225
1                                                        Met Lys    2

226  GTT CTA ATC TCT TCC CTC CTC CTG TTG CTG CCA CTA ATG CTG ATG  270
3    Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met Leu Met   17

271  TCC ATG GTC TCT AGC AGC CTG AAT CCA GGG GTC GCC AGA GGC CAC  315
18   Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg Gly His   32

316  AGG GAC CGA GGC CAG GCT TCT AGG AGA TGG CTC CAG GAA GGC GGC  360
33   Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly   47

361  CAA GAA TGT GAG TGC AAA GAT TGG TTC CTG AGA GCC CCG AGA AGA  405
48   Gln Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg   62

406  AAA TTC ATG ACA GTG TCT GGG CTG CCA AAG AAG CAG TGC CCC TGT  450
63   Lys Phe Met Thr Val Ser Gly Leu Pro Lys Lys Gln Cys Pro Cys   77

451  GAT CAT TTC AAG GGC AAT GTG AAG AAA ACA AGA CAC CAA AGG CAC  495
78   Asp His Phe Lys Gly Asn Val Lys Lys Thr Arg His Gln Arg His   92

496  CAC AGA AAG CCA AAC AAG CAT TCC AGA GCC TGC CAG CAA TTT CTC  540
93   His Arg Lys Pro Asn Lys His Ser Arg Ala Cys Gln Gln Phe Leu  107

541  AAA CAA TGT CAG CTA AGA AGC TTT GCT CTG CCT TTG TAG GAGCTCT  586
108  Lys Gln Cys Gln Leu Arg Ser Phe Ala Leu Pro Leu ***         119

587  GAGCGCCCACTCTTCCAATTAAACATTCTCAAAAAGCATGTTTTTCAAGATCATTTTGT  645
646  TTGTTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTAC  704
705  CCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGT  763
764  CATTTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAA  822
823  TGTCACAGAAAAAAAAAAAAAAAAAAAA                                  849
```

Fig. 2

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  1 ATTAAATTGTGCGCACACTACGCCACCTGAGCAGTGACAGGAAATCAGAAGCCTCTCGCT     60
 61 GGTGACAGTCCCCCACAGTCCTTAAGAAACAGCAGACAGCCGCA ATG AAG CTT CTA   116
  1                                              Met Lys Leu Leu     4

117  GCC TCT CCC TTC CTT CTG TTG CTG ACA GGG ATG TTC ACG GCC ACG    161
  5  Ala Ser Pro Phe Leu Leu Leu Leu Thr Gly Met Phe Thr Ala Thr     19

162  GTC TCC AGC AGC CCG AAT CAA GAG GTC GCC AGA CAC CAT GGG GAT    206
 20  Val Ser Ser Ser Pro Asn Gln Glu Val Ala Arg His His Gly Asp     34

207  CAA CAC CAG GCT CCT AGG AGG TGG CTC TGG GAA GGT GGC CAA GAG    251
 35  Gln His Gln Ala Pro Arg Arg Trp Leu Trp Glu Gly Gly Gln Glu     49

252  TGT GAC TGC AAA GAT TGG TCC CTG CGA GTC TCA AAG AGA AAA ACC    296
 50  Cys Asp Cys Lys Asp Trp Ser Leu Arg Val Ser Lys Arg Lys Thr     64

297  ACA GCA GTG CTG GAG CCA CCA AGG AAG CAG TGT CCC TGT GAT CAT    341
 65  Thr Ala Val Leu Glu Pro Pro Arg Lys Gln Cys Pro Cys Asp His     79

342  GTC AAG GGC AGT GAG AAA AAG AAC AGA CGC CAA AAG CAC CAC AGG    386
 80  Val Lys Gly Ser Glu Lys Lys Asn Arg Arg Gln Lys His His Arg     94

387  AAG TCA CAA AGG CCC TCC AGA ACC TGC CAG CAA TTT CTC AAG CGA    431
 95  Lys Ser Gln Arg Pro Ser Arg Thr Cys Gln Gln Phe Leu Lys Arg    109

432  TGT CAA CTA GCA AGC TTC GCC CTG CCC TTA TAG TTCCGAGACTCTGCC    479
110  Cys Gln Leu Ala Ser Phe Ala Leu Pro Leu ***                    119

480 CTCCAGCTAGGCTCTCTCAATGAGAGGGAGATGATCATCCTTGGAGCGCTTCTTATCCCC    539
540 CCACCCCCATCCTCACCAAGAGCACCCCAGCGCTCTCGAAGGCACGGCCCAGCTGTGTAC    599
600 CTGCCACTGTGTCCTCTGCACTTGTCACTCTTCTTACATGCCTTCTGTCCGGGGTCTAAA    659
660 AGGCAGGTGAAGCACTGAATCAGAGACTGCCTGGTTAGAAGCAATAAAGGTTTAGAAATT    719
720 GTGGTTTCTTAGCATCTAGACAACCTTCAGTGTTTATGGTTCCTGTCATCATCATCATCA    779
780 TCACCACCACCCTCATCACTACCCCCATCATTATCACTGCACTCTGTGGGTCTCTAACAC    839
840 AGTACAAGAGATATAAATGCAGAAGCACAGCTCGAGGCTAGAAAGATGGAAAGGAGGATC    899
900 CCAGCTGCCATTCAAAAGGGTTTTGAACCAATAAAAACAGAATGGCATCCGCAAAAAAAA    959
```

Fig. 3

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  1 AGCAGTTACAAGAAATCAGAAGCCTCTAACTGGTGACAATCCACACAGCCTTTAAGAACC    60

 61 AACAGACAGCC ACA ATG AAG CTT CTA GCC TCT CCC TTC CTT CTG TTG    107
  1                 Met Lys Leu Leu Ala Ser Pro Phe Leu Leu Leu     11
                                                ↓
108 CTT CCA GTG ATG CTC ATG TCC ATG GTC TTC AGC AGC CCG AAC CCA    152
 12 Leu Pro Val Met Leu Met Ser Met Val Phe Ser Ser Pro Asn Pro     26

153 GGG GTC GCC AGA AGC CAC GGG GAC CAA CAC CTG GCT CCT AGG AGG    197
 27 Gly Val Ala Arg Ser His Gly Asp Gln His Leu Ala Pro Arg Arg     41

198 TGG CTC TTG GAA GGT GGC CAA GAA TGT GAA TGC AAA GAT TGG TTC    242
 42 Trp Leu Leu Glu Gly Gly Gln Glu Cys Glu Cys Lys Asp Trp Phe     56

243 CTG CAA GCC CCA AAG AGA AAA GCC ACA GCA GTG CTG GGG CCA CCA    287
 57 Leu Gln Ala Pro Lys Arg Lys Ala Thr Ala Val Leu Gly Pro Pro     71

288 AGG AAG CAG TGT CCC TGT GAT CAC GTC AAG GGC AGG GAG AAA AAA    332
 72 Arg Lys Gln Cys Pro Cys Asp His Val Lys Gly Arg Glu Lys Lys     86

333 AAC AGA CAC CAA AAG CAC CAC AGG AAG TCG CAA AGA CCC TCC AGA    377
 87 Asn Arg His Gln Lys His His Arg Lys Ser Gln Arg Pro Ser Arg    101

378 GCC TGC CAG CAA TTT CTC AAA CGA TGT CAC CTG GCA AGC TTT GCG    422
102 Ala Cys Gln Gln Phe Leu Lys Arg Cys His Leu Ala Ser Phe Ala    116

423 CTG CCC TTA TAG TACTGAGACTCTGCTCCTCTAGTTAGACTCTCTCAGTGGAAAGG   478
117 Leu Pro Leu ***                                                 119

479 AGGTGACCAGCCCTAGCACGGTTCTTATTCTCCCCACCCCCATCCTCACCAAGAGCACCC    538
539 CAGTGCTCTCTGAAGGCACTGCCTCACAGTGTATCTATGACTGTGCCCCTAGTGCCGGCT    598
599 GCACTTGCCACTCTTGTCTTATGCCTTCTGTTTACCCTACAAGAATGCAGGACACCTCGG    658
659 CCTCCTGTTGGCCTCACATTGCAATCAGAAAACTTGCAATGAAAATAATTAAATACATAG    718
719 TGCATACGTGTGTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA                  764
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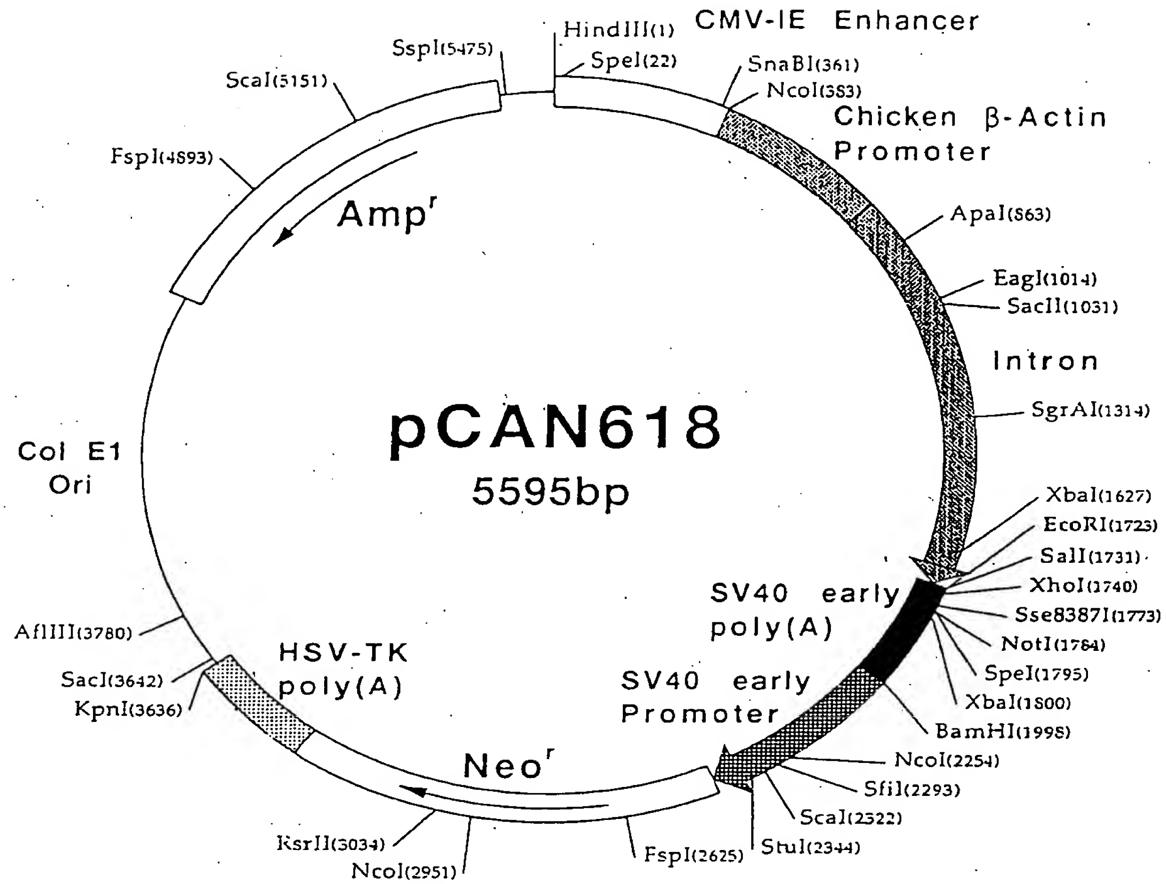
Fig. 4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EagI(1014)
SacII(1031)
Intron
SgrAI(1314)
XbaI(1627)
EcoRI(1723)
SalI(1731)
XhoI(1740)
Sse8387I(1773)
NotI(1784)
SpeI(1795)
XbaI(1800)
BamHI(1998)
NcoI(2254)
SfiI(2293)
ScaI(2522)
StuI(2344)
FspI(2625)
SV40 early
poly(A)
SV40 early
Promoter
Neo^r
NcoI(2951)
KsrII(3034)
HSV-TK
poly(A)
KpnI(3636)
SacI(3642)
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Amp^r
FspI(4893)
ScaI(5151)
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Fig. 5

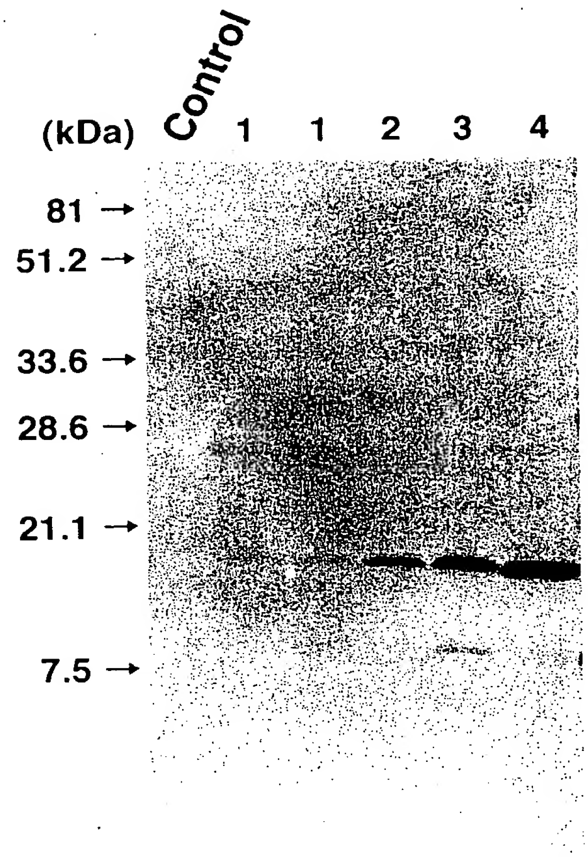
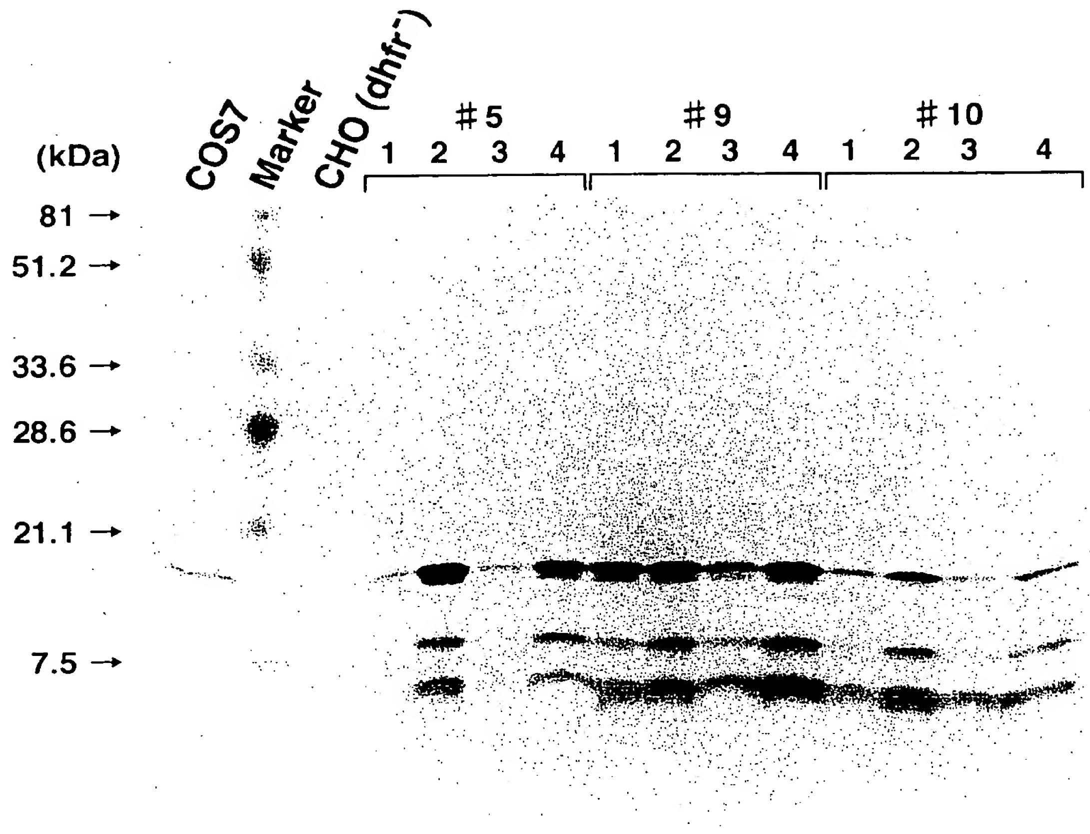


Fig. 6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COS7
Marker
CHO (dhfr⁻)
#5
#9
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1 2 3 4 1 2 3 4 1 2 3 4
81
51.2
33.6
28.6
21.1
7.5

Fig. 7